**Overall description:**

**2.1** **Product Perspective**

During clinical diagnosis, the patients’ genetic information is considered as a factor that influences drug choosing. A clinical report that contains the patients’ genetic variant information and related drugs can help doctors avoiding improper drug choosing in clinical diagnosis, significantly. The *product* is based on a database that contains gene, genetic variant and drug information. With the patients’ genetic information as input, the *product* can provide detailed information about the patients’ variants and related drug.

The *product* can be divided into two parts, database and web interface. The database contains the collection of gene, genetic variant and drug information. The information is stored in the different tables respectively. The data will be collected from the pharmGKB database and be organized by PostgreSQL. The SQL queries will be written for detailed information searching. The web interface will be built by Java. The users will be able to submit fastq file that contains patients as the input query. The file will then be sent to the server and generate a vcf file that stores the patient’s genetic variant information. The variant information will then be put into a filtering algorism to filtrate the relevant information. Finally, the relevant information will be used as queries to search for related drug information in the database and all information will be sent back to the web interface and generate a clinical report for the user.

**2.2 Product Functionality**

Provide a clinical report that contains related drugs according to user submitted genetic information

**2.3 Users and Characteristics**

Doctors:

Will use the software frequently.

Will use the clinical report as the reference for drug using.

The query is the fastq file that contains the patient’s genetic information

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**2.4 Operating Environment**

We will be using Github for our repository. The code will be developed on our personal computers and *sent to the server (not sure).* The database will be generating and operating by PostgreSQL. The web interface will be built by Java.

**2.5 Design and Implementation Constraints**

I don’t Know

Software specifications

PostgreSQL

Java SDK 11+

JetBrains IDEA or Eclipse (IDE)

Servlet & JSP (dynamic webpage)

JSTL (template)

SLF4J (logging framework)

Gson (data passing mechanism)

**2.6 User Documentation**

A user manual explaining what the functionality and usage of the visualization software will be required. The detailed information about how to use the software will be posted on the web interface

**2.7 Assumption and Dependencies**

We assume that all users can provide a fastq file with good quality as the genetic information input.